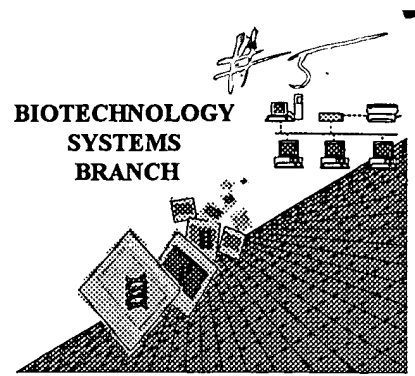


0308

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/399,492
Art Unit / Team No. : 01PE
Date Processed by STIC: 10/5/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/399,492

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xI) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/399,492

DATE: 10/05/1999
TIME: 10:44:46

Input Set: I399492.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: Bazan, J. Fernando
2 <120> TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
3 <130> FILE REFERENCE: DX0903K
4 <140> CURRENT APPLICATION NUMBER: US/09/399,492
5 <141> CURRENT FILING DATE: 1999-09-20
6 <160> NUMBER OF SEQ ID NOS: 9
7 <170> SOFTWARE: PatentIn Ver. 2.0
8 <210> SEQ ID NO 1
9 <211> LENGTH: 468
10 <212> TYPE: DNA
11 <213> ORGANISM: primate
12 <220> FEATURE:
13 <221> NAME/KEY: misc_feature
14 <222> LOCATION: (301)
15 <223> OTHER INFORMATION: nucleotide may be A, C, G, or T
16 <220> FEATURE:
17 <221> NAME/KEY: CDS
18 <222> LOCATION: (20)..(466)
19 <220> FEATURE:
20 <221> NAME/KEY: mat_peptide
21 <222> LOCATION: (119)..(466)
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25 -30 -25
26 cta tat gtt ctg tca gtt tct ttc agg aaa atc ttc atc tta caa ctt 100
27 Leu Tyr Val Leu Ser Val Ser Phe Arg Lys Ile Phe Ile Leu Gln Leu
28 -20 -15 -10
29 gta ggg ctg gtg tta act tac gac ttc act aac tgt gac ttt gag aag 148
30 Val Gly Leu Val Leu Thr Tyr Asp Phe Thr Asn Cys Asp Phe Glu Lys
31 -5 -1 1 5 10
32 att aaa gca gcc tat ctc agt act att tct aaa gac ctg att aca tat 196
33 Ile Lys Ala Ala Tyr Leu Ser Thr Ile Ser Lys Asp Leu Ile Thr Tyr
34 15 20 25
35 atg agt ggg acc aaa agt acc gag ttc aac aac acc gtc tct tgt agc 244
36 Met Ser Gly Thr Lys Ser Thr Glu Phe Asn Asn Thr Val Ser Cys Ser
37 30 35 40
38 aat cgg cca cat tgc ctt act gaa atc cag agc cta acc ttc aat ccc 292
39 Asn Arg Pro His Cys Leu Thr Glu Ile Gln Ser Leu Thr Phe Asn Pro
40 45 50 55
41 aac cgc cgn gtg cgg tcg ctc gcc aaa gaa atg ttc gcc atg aaa act 340
42 Asn Arg Xaa Val Arg Ser Leu Ala Lys Glu Met Phe Ala Met Lys Thr
43 60 65 70
44 aag gct gcc tta gct atc tgg tgc cca ggc tat tcg gaa act cag ata 388

Does Not Comply
Corrected Diskette Needed

W
P2

W-->OK

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/399,492

DATE: 10/05/1999

TIME: 10:44:46

Input Set: I399492.RAW

45 Lys Ala Ala Leu Ala Ile Trp Cys Pro Gly Tyr Ser Glu Thr Gln Ile
46 75 80 85 90
47 aat gct act cag gca atg aag aag agg aga aaa agg aaa gtc aca acc 436
48 Asn Ala Thr Gln Ala Met Lys Lys Arg Arg Lys Arg Lys Val Thr Thr
49 95 100 105
50 aat aaa tgt ctg gaa caa gtg tca caa tta aa 468
51 Asn Lys Cys Leu Glu Gln Val Ser Gln Leu
52 110 115

53 <210> SEQ ID NO 2

54 <211> LENGTH: 149

55 <212> TYPE: PRT

56 <213> ORGANISM: primate

57 <400> SEQUENCE: 2

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59 -30 -25 -20
60 Val Ser Phe Arg Lys Ile Phe Ile Leu Gln Leu Val Gly Leu Val Leu
61 -15 -10 -5
62 Thr Tyr Asp Phe Thr Asn Cys Asp Phe Glu Lys Ile Lys Ala Ala Tyr
63 -1 1 5 10 15
64 Leu Ser Thr Ile Ser Lys Asp Leu Ile Thr Tyr Met Ser Gly Thr Lys
65 20 25 30
66 Ser Thr Glu Phe Asn Asn Thr Val Ser Cys Ser Asn Arg Pro His Cys
67 35 40 45
68 Leu Thr Glu Ile Gln Ser Leu Thr Phe Asn Pro Asn Arg Xaa Val Arg
69 50 55 60
70 Ser Leu Ala Lys Glu Met Phe Ala Met Lys Thr Lys Ala Ala Leu Ala
71 65 70 75
72 Ile Trp Cys Pro Gly Tyr Ser Glu Thr Gln Ile Asn Ala Thr Gln Ala
73 80 85 90 95
74 Met Lys Lys Arg Arg Lys Arg Lys Val Thr Thr Asn Lys Cys Leu Glu
75 100 105 110
76 Gln Val Ser Gln Leu
77 115

78 <210> SEQ ID NO 3

79 <211> LENGTH: 480

80 <212> TYPE: DNA

81 <213> ORGANISM: primate

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84 <222> LOCATION: (1)..(477)

85 <220> FEATURE:

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87 <222> LOCATION: (85)..(477)

88 <400> SEQUENCE: 3

89 atg ttc cct ttt gcc tta cta tat gtt ctg tca gtt tct ttc agg aaa 48
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91 -25 -20 -15
92 atc ttc atc tta caa ctt gta ggg ctg gtg tta act tac gac ttc act 96
93 Ile Phe Ile Leu Gln Leu Val Gly Leu Val Leu Thr Tyr Asp Phe Thr
94 -10 -5 -1 1

W-->

see item 10
in Enon
summary
sheet

DATE: 10/05/1999
TIME: 10:44:46

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 95 | aac | tgt | gac | ttt | gag | aag | att | aaa | gca | gcc | tat | ctc | agt | act | att | tct | 144 |
| 96 | Asn | Cys | Asp | Phe | Glu | Lys | Ile | Lys | Ala | Ala | Tyr | Leu | Ser | Thr | Ile | Ser | |
| 97 | 5 | | | | | 10 | | | | | 15 | | | | | 20 | |
| 98 | aaa | gac | ctg | att | aca | tat | atg | agt | ggg | acc | aaa | agt | acc | gag | ttc | aac | 192 |
| 99 | Lys | Asp | Leu | Ile | Thr | Tyr | Met | Ser | Gly | Thr | Lys | Ser | Thr | Glu | Phe | Asn | |
| 100 | | | | | 25 | | | | | 30 | | | | | 35 | | |
| 101 | aac | acc | gtc | tct | tgt | agc | aat | cgg | cca | cat | tgc | ctt | act | gaa | atc | cag | 240 |
| 102 | Asn | Thr | Val | Ser | Cys | Ser | Asn | Arg | Pro | His | Cys | Leu | Thr | Glu | Ile | Gln | |
| 103 | | | | | 40 | | | | | 45 | | | | | 50 | | |
| 104 | agc | cta | acc | ttc | aat | ccc | acc | gcc | ggc | tgc | gcg | tcg | ctc | gcc | aaa | gaa | 288 |
| 105 | Ser | Leu | Thr | Phe | Asn | Pro | Thr | Ala | Gly | Cys | Ala | Ser | Leu | Ala | Lys | Glu | |
| 106 | | | | | 55 | | | | 60 | | | | | | 65 | | |
| 107 | atg | ttc | gcc | atg | aaa | act | aag | gct | gcc | tta | gct | atc | tgg | tgc | cca | ggc | 336 |
| 108 | Met | Phe | Ala | Met | Lys | Thr | Lys | Ala | Ala | Leu | Ala | Ile | Trp | Cys | Pro | Gly | |
| 109 | | | | | 70 | | | | 75 | | | | 80 | | | | |
| 110 | tat | tcg | gaa | act | cag | ata | aat | gct | act | cag | gca | atg | aag | aag | agg | aga | 384 |
| 111 | Tyr | Ser | Glu | Thr | Gln | Ile | Asn | Ala | Thr | Gln | Ala | Met | Lys | Lys | Arg | Arg | |
| 112 | 85 | | | | | 90 | | | | | 95 | | | | | 100 | |
| 113 | aaa | agg | aaa | gtc | aca | acc | aat | aaa | tgt | ctg | gaa | caa | gtg | tca | caa | tta | 432 |
| 114 | Lys | Arg | Lys | Val | Thr | Thr | Asn | Lys | Cys | Leu | Glu | Gln | Val | Ser | Gln | Leu | |
| 115 | | | | | 105 | | | | | 110 | | | | | 115 | | |
| 116 | caa | gga | ttg | tgg | cgt | cgc | ttc | aat | cga | cct | tta | ctg | aaa | caa | cag | taa | 480 |
| 117 | Gln | Gly | Leu | Trp | Arg | Arg | Phe | Asn | Arg | Pro | Leu | Leu | Lys | Gln | Gln | | |
| 118 | | | | | 120 | | | | | 125 | | | | | 130 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 124 | Met | Phe | Pro | Phe | Ala | Leu | Leu | Tyr | Val | Leu | Ser | Val | Ser | Phe | Arg | Lys |
| 125 | | | | -25 | | | | | -20 | | | | | -15 | | |
| 126 | Ile | Phe | Ile | Leu | Gln | Leu | Val | Gly | Leu | Val | Leu | Thr | Tyr | Asp | Phe | Thr |
| 127 | | | -10 | | | | | -5 | | | | -1 | 1 | | | |
| 128 | Asn | Cys | Asp | Phe | Glu | Lys | Ile | Lys | Ala | Ala | Tyr | Leu | Ser | Thr | Ile | Ser |
| 129 | 5 | | | | | 10 | | | | | 15 | | | | | 20 |
| 130 | Lys | Asp | Leu | Ile | Thr | Tyr | Met | Ser | Gly | Thr | Lys | Ser | Thr | Glu | Phe | Asn |
| 131 | | | | 25 | | | | | | 30 | | | | | 35 | |
| 132 | Asn | Thr | Val | Ser | Cys | Ser | Asn | Arg | Pro | His | Cys | Leu | Thr | Glu | Ile | Gln |
| 133 | | | 40 | | | | | | 45 | | | | | 50 | | |
| 134 | Ser | Leu | Thr | Phe | Asn | Pro | Thr | Ala | Gly | Cys | Ala | Ser | Leu | Ala | Lys | Glu |
| 135 | | | 55 | | | | | 60 | | | | | 65 | | | |
| 136 | Met | Phe | Ala | Met | Lys | Thr | Lys | Ala | Ala | Leu | Ala | Ile | Trp | Cys | Pro | Gly |
| 137 | | 70 | | | | | 75 | | | | | 80 | | | | |
| 138 | Tyr | Ser | Glu | Thr | Gln | Ile | Asn | Ala | Thr | Gln | Ala | Met | Lys | Lys | Arg | Arg |
| 139 | 85 | | | | | 90 | | | | | 95 | | | | | 100 |
| 140 | Lys | Arg | Lys | Val | Thr | Thr | Asn | Lys | Cys | Leu | Glu | Gln | Val | Ser | Gln | Leu |
| 141 | | | | 105 | | | | | | 110 | | | | | 115 | |
| 142 | Gln | Gly | Leu | Trp | Arg | Arg | Phe | Asn | Arg | Pro | Leu | Leu | Lys | Gln | Gln | |
| 143 | | | | 120 | | | | | 125 | | | | | 130 | | |

144 <210> SEQ ID NO 5

PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/399,492

DATE: 10/05/1999
TIME: 10:44:46

Input Set: I399492.RAW

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145 <211> LENGTH: 176
146 <212> TYPE: PRT
147 <213> ORGANISM: artiodactyla
148 <400> SEQUENCE: 5
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151   Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Phe Ser Gly Lys
152               20             25             30
153   Asp Gly Gly Ala Tyr Gln Asn Val Leu Met Val Ser Ile Asp Asp Leu
154               35             40             45
155   Asp Asn Met Ile Asn Phe Asp Ser Asn Cys Leu Asn Asn Glu Pro Asn
156               50             55             60
157   Phe Phe Lys Lys His Ser Cys Asp Asp Asn Lys Glu Ala Ser Phe Leu
158               65             70             75             80
159   Asn Arg Ala Ala Arg Lys Leu Lys Gln Phe Leu Lys Met Asn Ile Ser
160               85             90             95
161   Asp Asp Phe Lys Leu His Leu Ser Thr Val Ser Gln Gly Thr Leu Thr
162               100            105            110
163   Leu Leu Asn Cys Thr Ser Lys Gly Lys Gly Arg Lys Pro Pro Ser Leu
164               115            120            125
165   Gly Glu Ala Gln Pro Thr Lys Asn Leu Glu Glu Asn Lys Ser Leu Lys
166               130            135            140
167   Glu Gln Arg Lys Gln Asn Asp Leu Cys Phe Leu Lys Ile Leu Leu Gln
168               145            150            155            160
169   Lys Ile Lys Thr Cys Trp Asn Lys Ile Leu Arg Gly Ile Thr Glu His
170               165            170            175
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172 <211> LENGTH: 176
173 <212> TYPE: PRT
174 <213> ORGANISM: artiodactyla
175 <400> SEQUENCE: 6
176   Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
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178   Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Ser Gly Lys
179               20             25             30
180   Asp Gly Gly Ala Tyr Gln Asn Val Leu Met Val Asn Ile Asp Asp Leu
181               35             40             45
182   Asp Asn Met Ile Asn Phe Asp Ser Asn Cys Leu Asn Asn Glu Pro Asn
183               50             55             60
184   Phe Phe Lys Lys His Ser Cys Asp Asp Asn Lys Glu Ala Ser Phe Leu
185               65             70             75             80
186   Asn Arg Ala Ser Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ile Ser
187               85             90             95
188   Asp Asp Phe Lys Leu His Leu Ser Thr Val Ser Gln Gly Thr Leu Thr
189               100            105            110
190   Leu Leu Asn Cys Thr Ser Lys Gly Lys Gly Arg Lys Pro Pro Ser Leu
191               115            120            125
192   Ser Glu Ala Gln Pro Thr Lys Asn Leu Glu Glu Asn Lys Ser Ser Lys
193               130            135            140
194   Glu Gln Lys Lys Gln Asn Asp Leu Cys Phe Leu Lys Ile Leu Leu Gln

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PAGE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/399,492

DATE: 10/05/1999
TIME: 10:44:46

Input Set: I399492.RAW

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196      Lys Ile Lys Thr Cys Trp Asn Lys Ile Leu Arg Gly Ile Lys Glu His
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199 <211> LENGTH: 177
200 <212> TYPE: PRT
201 <213> ORGANISM: primate
202 <400> SEQUENCE: 7
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204          1          5          10          15
205      Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Glu Gly Lys
206                      20          25          30
207      Asp Gly Lys Gln Tyr Glu Ser Val Leu Met Val Ser Ile Asp Gln Leu
208                      35          40          45
209      Leu Asp Ser Met Lys Glu Ile Gly Ser Asn Cys Leu Asn Asn Glu Phe
210          50          55          60
211      Asn Phe Phe Lys Arg His Ile Cys Asp Ala Asn Lys Glu Gly Met Phe
212          65          70          75          80
213      Leu Phe Arg Ala Ala Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ser
214                      85          90          95
215      Thr Gly Asp Phe Asp Leu His Leu Leu Lys Val Ser Glu Gly Thr Thr
216                      100          105          110
217      Ile Leu Leu Asn Cys Thr Gly Gln Val Lys Gly Arg Lys Pro Ala Ala
218          115          120          125
219      Leu Gly Glu Ala Gln Pro Thr Lys Ser Leu Glu Glu Asn Lys Ser Leu
220          130          135          140
221      Lys Glu Gln Lys Lys Leu Asn Asp Leu Cys Phe Leu Lys Arg Leu Leu
222          145          150          155          160
223      Gln Glu Ile Lys Thr Cys Trp Asn Lys Ile Leu Met Gly Thr Lys Glu
224                      165          170          175
225      His
226 <210> SEQ ID NO 8
227 <211> LENGTH: 154
228 <212> TYPE: PRT
229 <213> ORGANISM: rodent
230 <400> SEQUENCE: 8
231      Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
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233      Leu Val Leu Leu Pro Val Thr Ser Ser Glu Cys His Ile Lys Asp Lys
234                      20          25          30
235      Glu Gly Lys Ala Tyr Glu Ser Val Leu Met Ile Ser Ile Asp Glu Leu
236                      35          40          45
237      Asp Lys Met Thr Gly Thr Asp Ser Asn Cys Pro Asn Asn Glu Pro Asn
238          50          55          60
239      Phe Phe Arg Lys His Val Cys Asp Asp Thr Lys Glu Ala Ala Phe Leu
240          65          70          75          80
241      Asn Arg Ala Ala Arg Lys Leu Lys Gln Phe Leu Lys Met Asn Ile Ser
242                      85          90          95
243      Glu Glu Phe Asn Val His Leu Leu Thr Val Ser Gln Gly Thr Gln Thr
244                      100          105          110

```

VERIFICATION SUMMARY
PATENT APPLICATION US/09/399,492

DATE: 10/05/1999

TIME: 10:44:46

Input Set: I399492.RAW

Line ? Error/Warning

Original Text

41 W "N" or "Xaa" used: Feature required

aac cgc cgn gtg cgg tcg ctc gcc aaa gaa a

68 W "N" or "Xaa" used: Feature required

Leu Thr Glu Ile Gln Ser Leu Thr Phe Asn P